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Research Article

Two new species of *Entoloma* subg. *Cyanula* sect. *Asprella* (Entolomataceae, Agaricales) from subtropical regions of China

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Abstract

Two new species of *Entoloma* subg. *Cyanula*, *E. qingluan* and *E. zilin*, are described from subtropical regions of China based on morphological and phylogenetic evidence. *E. qingluan* is characterized by blue basidiomata, paler greyish-blue lamellae with a poliopus-type lamella edge, and pileipellis cells containing dark brown vacuolar pigments. *E. zilin* features a greyish-magenta scaly pileus with a bluish lamella edge adjacent to the stipe, a blue stipe, fertile lamella edges, and predominantly 2-spored basidia. Both species are assigned to subg. *Cyanula* sect. *Asprella* based on their striate or squamulose pileus, blue stipe, and fertile or poliopus-type lamella edge. Detailed descriptions, color photos, and scanning electron micrographs of spores are presented.

Key words: Basidiomycetes, new taxa, phylogeny, taxonomy

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Introduction

Entoloma (Fr.) P. Kumm. is a species-rich and morphologically diverse genus in the Agaricales Underw. (Kirk et al. 2008) and the largest genus in the Entolomataceae Kotl. & Pouzar. It is widely distributed across five continents, having been found in regions ranging from frigid Arctic zones to temperate areas and tropical regions. Most species of *Entoloma* are saprotrophic fungi, commonly thriving in shady and damp forest zones, on litter, as well as on soil and decaying wood. Additionally, some species are capable of parasitizing other fungi or plants (Horak 1980; Noordeloos 1981; Ediriweera et al. 2017). More than 2,000 species within this genus have been reported worldwide (Romagnesi 1941; Romagnesi and Gilles 1979; Horak 1980, 1982; Largent 1994; Horak 2008; Noordeloos and Gates 2012). The primary characteristics of this genus include spore prints ranging in color from pink, angular basidiospores observed from all angles, and remarkable morphological diversity, including mycenoid, collybioid, omphalioid, clitocyboid, and pleurotoid forms (Co-David et al. 2009; Baroni and Matheny 2011).

Historically, the taxonomic position of species within *Entoloma* subg. *Cyanula* has been debated. Romagnesi (1974) first treated them as a section within *Rhodophyllus* Quél. sensu lato. Later, they were transferred to *Entoloma*

subg. *Leptonia*, which was divided into three sections: sect. *Leptonia*, sect. *Cyanula*, and sect. *Griseorubida* (Noordeloos 2004; Noordeloos and Gates 2012). However, subsequent molecular phylogenetic studies revealed that subg. *Leptonia* is polyphyletic. Specifically, sect. *Leptonia* belongs to the */Nolanea–Claudopus* clade, whereas sect. *Cyanula* and sect. *Griseorubida* fall within the */Inocephalus–Cyanula* clade (Co-David et al. 2009; Noordeloos and Gates 2012; Largent et al. 2016). Morphologically, species within sect. *Leptonia* exhibit clamp connections, whereas those in sect. *Cyanula* lack such structures. Based on molecular and morphological evidence, sect. *Cyanula* was elevated to the rank of subgenus (Noordeloos and Gates 2012; Reschke et al. 2022a). In the monograph of Noordeloos et al. (2022a), the authors reclassified species with a striate or squamulose pileus, blue stipe, and either fertile lamellae edge or sterile, poliopus-type lamella edge into sect. *Asprella* of subg. *Cyanula*. The section can be divided into six subsections, namely, subsect. *Asprella*, subsect. *Exilia*, subsect. *Cistocruentata*, subsect. *Cyaneoliacina*, subsect. *Rivipollensia*, and subsect. *Perfidodisca*.

Taxonomic studies on species within subg. *Cyanula* remain limited in China. To date, only 17 taxa within subg. *Cyanula* have been documented in China, including four species newly described in recent studies (Chen et al. 2025). Over the past few years, during our investigations into macrofungal diversity in subtropical regions of China, we have found that species within subg. *Cyanula* exhibit remarkably high diversity, with numerous potentially undescribed taxa. This study describes two novel species within subg. *Cyanula* sect. *Asprella*, based on comparative morphological characterization and phylogenetic analyses.

Materials and methods

Morphological studies

The specimens in this study were collected from Fujian and Zhejiang Provinces in China between 2022 and 2023 and were preserved as dried specimens. All specimens are deposited in the Herbarium of Fungi, Jiangxi Agricultural University (HFJAU). Fresh specimens were photographed in the field and recorded macroscopically. Color notations adhered to the Methuen Handbook of Colour (Kornerup and Wanscher 1978). Micromorphological structures were observed and measured under an Olympus BX53 microscope (Olympus Corporation, Tokyo, Japan) by making squash preparations of sections of dried specimens that were placed in 5% KOH solution or H_2O. A 1% Congo red solution was used as the staining agent for observing colorless tissues. Amyloidity was tested with Melzer's reagent (Horak 2005; Chen et al. 2024). For each collection, the dimensions of at least 40 basidiospores, basidia, and cystidia were measured. The size range of spores is expressed in the format (a) b–c (d), where "a" and "d" represent the minimum and maximum values, respectively, and 90% of the spores fall within the range of "b–c." The meanings of other spore characteristics are as follows: "Q" represents the length-to-width ratio; "av" indicates the average value; "n" denotes the number of measurements; and "Qm" represents the average "Q" value ± standard deviation (Yu et al. 2020). Morphological descriptions are based on the work of Noordeloos et al. (2022a). The morphology of the spores was further verified

using an electron microscope. A portion of the gills from the dried fruiting body was sampled and observed under an electron microscope (JEOL JSM-IT800 Schottky Field Emission Scanning Electron Microscope).

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from dried specimens using the NuClean Plant Genomic DNA kit (CWBIO, China) (Wang et al. 2022). The nrDNA ITS and LSU regions were amplified using the primer pairs ITS1F/ITS4 and LR0R/LR5 or LR7 (White et al. 1990; Hopple and Vilgalys 1999).

PCR amplification was conducted using a 25 µL reaction system as follows: 1 µL of DNA, 1 µL of each forward and reverse primer, 9.5 µL of ddH_2O, and 12.5 µL of 2× TaqMaster Mix [Qing Ke Biotechnology Co. Ltd. (Wuhan City, China)]. PCR was performed using a touchdown program for all regions: initial 95 °C for 5 min; 14 cycles of denaturing at 95 °C for 30 s, annealing at 65 °C for 45 s (with a decrease of 1 °C per cycle), and extension at 72 °C for 1 min; followed by 30 cycles of denaturing at 95 °C for 30 s, annealing at 52 °C for 30 s, and extension at 72 °C for 1 min; and a final extension at 72 °C for 10 min (Bau and Yan 2021). The PCR products were sequenced by Qing Ke Biotechnology Co. Ltd. (Wuhan City, China).

Alignment and phylogenetic analyses

A total of 89 sequences (62 ITS sequences and 27 LSU sequences) from 62 samples were used for phylogenetic analyses using Bayesian inference (BI) and maximum likelihood (ML). Sequence selection was based on the results of BLAST for ITS and the study of Noordeloos et al. (2022a). Species of *E.* subg. *Cubospora* served as outgroups (Table 1). ITS and LSU sequences were aligned separately with the MAFFT online server using the automatic selection of algorithm (Katoh et al. 2019). Concatenated sequences were analyzed with MRBAYES v.3.2.7a (Ronquist et al. 2012) and IQ-TREE v.2.1.2 (Nguyen et al. 2015), respectively. For the ML analysis, models of sequence evolution were assessed in IQ-TREE prior to analysis, allowing partitions of the sequences to have different seeds (-spp). The selected models were TPM2u+F+I+G4 for ITS and TPM3u+F+I+G4 for LSU. Ultrafast bootstrap support values were calculated from 1,000 replicates. For the BI analysis, the Markov chain Monte Carlo runs were set for 2 million generations. The first 25% of trees were discarded as burn-in. Nodes with Bayesian posterior probabilities (BI-PP) ≥ 0.95 and ML ultrafast bootstrap proportions (ML-BP) ≥ 95% were considered statistically supported (Nguyen et al. 2015).

Results

Phylogenetic analysis

A total of 1,715 characters were used in the phylogenetic analyses (ITS, 827 bp; LSU, 888 bp), of which 991 were constant, 554 were parsimony-informative, and 170 were singleton. For the Bayesian analysis, the average standard deviation of split frequencies was less than 0.01 after 1,625,000 generations.

The result of the phylogenetic analysis is shown in Fig. 1. The two new species were clustered in subg. *Cyanula* sect. *Asprella* and formed separate and

Table 1. Details of sequences used in the phylogenetic analyses. Newly generated sequences were in bold.

Species	Location	Voucher Number	ITS	LSU	Sequence origin
Entoloma argus	Vietnam	LE F-312694 holotype	OM987263	OM996175	(Morozova et al. 2022)
E. arion	Vietnam	LE F-312691 holotype	OM987259	OM996176	(Morozova et al. 2022)
E. asprellum	Estonia	TUF106064	UDB011486	—	UNITE
E. azureosquamulosum	China	GDGM27355 holotype	NR_137086	NG_059214	(He et al. 2012)
E. caespitosum	China	GDGM24025	JQ281490	JQ410327	(He et al. 2012)
E. caespitosum	China	GDGM24026	JQ281491	JQ320133	(He et al. 2012)
E. calceus	Norway	O-F-259457 holotype	NR_182489	—	(Noordeloos et al. 2022b)
E. calceus	France	LIP0402265	ON008492	—	(Noordeloos et al. 2022b)
E. callipygmaeum	Russia	LE253784 holotype	MZ145207	—	(Dima et al. 2021)
E. carneogriseum	Norway	O-F-256479	UDB07673714	—	UNITE
E. chalybeum	Russia	LE254353	KC898445	KC898500	(Morozova et al. 2014)
E. chalybeum	Denmark	TUF105760	UDB034191	—	UNITE
E. chloropolium	Estonia	TUF120516	UDB031513	—	UNITE
E. cistocruentatum	Spain	L 0607521	NR_182485	—	(Noordeloos et al. 2022b)
E. coracis	Norway	O-F-256850 holotype	MW934571	MW934251	(Crous et al. 2021b)
E. corvinum	France	FA4261	OR419868	—	(Armada et al. 2023)
E. cyaneolilacinum	Norway	O-F-252009 holotype	MW934582	MW934252	(Crous et al. 2021b)
E. cyanostipitum	China	GDGM31318 holotype	KY711237	KY972694	(He et al. 2017)
E. cycneum	Vietnam	LE F-343654 holotype	OQ779461	OQ804518	(Morozova and Pham 2023)
E. dislocatum	Spain	L0607565 holotype	ON008483	—	(Noordeloos et al. 2022b)
E. exile	Germany	Lueck8	KP965773	KP965791	(Karich et al. 2015)
E. exile	USA	K(M)187354	MF977976	—	Unpublished in GenBank
E. griseocyaneum	Russia	LE254351	KC898444	KC898498	(Morozova et al. 2014)
E. griseocyaneum	Germany	KaiR997	MZ611684	—	(Reschke et al. 2022b)
E. icarus	Vietnam	LE F-312696 holotype	OM987257	OM996174	(Morozova et al. 2022)
E. incanum	Sweden	LE312503 neotype	OK161247	OK161275	(Crous et al. 2021b)
E. incanum	Russia	LE311794	OK161249	OK161276	(Crous et al. 2021b)
E. isborscanum	Russia	LE302088 holotype	MW934566	MW934253	(Crous et al. 2021a)
E. kovalenkoi	Vietnam	LE312529 holotype	OK257210	OK257207	(He et al. 2014)
E. linkii	Norway	O-F-256353	UDB07673651	—	UNITE
E. mastoideum	China	GDGM28820	JQ281476	JQ410328	(He et al. 2012)
E. meridionale	Greece	ACAM2018-0153 holotype	OL679700	—	(Dima et al. 2022)
E. mougeotii	Estonia	TUF101633	UDB016265	—	UNITE
E. mougeotii	Estonia	TUF106505	UDB019720	—	UNITE
E. murrayi	China	QI 1001	KJ658967	JQ993090	(He et al. 2014)
E. mutabilipes	Finland	TUR610/12	LN850550	—	(Kokkonen 2015)
E. notabile	Cyprus	L-0607514 holotype	OL343537	—	(Vila et al. 2021)
E. pallidostriatum	Spain	L-0607566 holotype	NR_177630	—	(Vila et al. 2021)
E. perasprellum	France	GC01100310 holotype	MZ145177	—	(Dima et al. 2021)
E. perchalybeum	Sweden	GB-0209474 holotype	NR_182490	—	(Noordeloos et al. 2022b)
E. perfidodiscum	Spain	L-0607586 holotype	NR_177633	—	(Vila et al. 2021)
E. phlebophyllum	China	HFJAU3126	OR827451	OR826040	(Chen et al. 2024)

Species	Location	Voucher Number	ITS	LSU	Sequence origin
E. poliopus	Estonia	TUF120264	UDB024655	—	UNITE
E. pseudosubcorvinum	Thailand	SDBR-CMUNK0985 holotype	MZ215769	MZ203540	(Bhunjun et al. 2022)
E. pulchripes	Russia	LE311808 holotype	MZ145188	—	(Dima et al. 2021)
E. pulchripes	Russia	LE311809	MZ145189	—	(Dima et al. 2021)
E. qingluan	**China**	**HFJAU5122 holotype**	**PX426788**	**PX426795**	**This work**
E. qingluan	**China**	**HFJAU5723**	**PX426789**	**PX426796**	**This work**
E. queletii	Turkey	OKA-TR1002	MT741747	—	Unpublished in GenBank
E. queletii	Estonia	TUF141044	UDB07674927	—	UNITE
E. riparium	Italy	L-0607563 holotype	NR_177632	—	(Vila et al. 2021)
E. rivipollense	Spain	L-0607585 holotype	NR_177634	—	(Vila et al. 2021)
E. septentrionale	Norway	O-F-254295 holotype	NR_174647	—	(Noordeloos et al. 2021)
E. serrulatum	Russia	LE254361	KC898447	KC898501	(Morozova et al. 2014)
E. serrulatum	Iran	EnSe-1	KT833862	—	Unpublished in GenBank
E. sicoense	Portugal	PO-F2244 holotype	OR026624	—	(Fachada et al. 2023)
E. sicoense	Portugal	PO-F2245	OR026625	—	(Fachada et al. 2023)
E. subcaesiocinctum	China	SAAS133 holotype	KY711236	KY972697	(He et al. 2017)
E. subtenuicystidiatum	China	GDGM 28459 holotype	JQ320109	JQ320116	(He et al. 2012)
E. timidum	Russia	LE 312480 holotype	MZ145197	—	(Dima et al. 2021)
E. turci	Austria	WU25055	UDB0802163	—	UNITE
E. zilin	**China**	**HFJAU3354 holotype**	**PX426790**	**PX426797**	**This work**

well-supported branches. *E. qingluan* formed a separate and well-supported lineage (BI-PP = 1, ML-BP = 100%) and grouped with *E. exile* (Fr.) Hesler. *E. zilin* belongs to /sect. *Asprella* subsect. *Cyaneolilacina* and is closely related to *E. cyaneolilacinum*.

Taxonomy

Entoloma qingluan **J.Q. Yan, Y.Q. Xu & S.N. Wang, sp. nov.**
MycoBank No: 860910
Fig. 2

Etymology. Derived from Hanyu Pinyin, the epithet alludes to the Qingluan bird of the *Classic of Mountains and Seas*, whose plumage matches the fungus's color.

Chinese name. 青鸾粉褶菌.

Holotype. China • Fujian Province, Wuyishan, 16 August 2023, collected by Nian-kai Zeng, Cheng-feng Nie, Hua-zhi Qin, Hui Deng, Tian Jiang, Run-xiang Zhao, HFJAU5122.

Diagnosis. *Entoloma qingluan* is mainly characterized by the rather small, tricholomatoid basidiomata; a convex, bluish grey to blackish blue pileus; paler greyish blue lamellae with sterile lamellae edge; narrow clavate cheilocystidia, and pileipellis cells containing dark brown vacuolar pigments; clamp connections absent.

Macromorphology. Basidiomata rather small, tricholomatoid. Pileus 6.0–8.0 mm wide, convex, slightly umbonate, bluish grey to blackish blue (20F3–5), darker at center, paler toward margin, margin entire, slightly involute. Lamellae

Entoloma calceus Norway O-F-259457 holotype
Entoloma calceus France LIP0402265
Entoloma corvinum France FA4261
Entoloma perchalybeum Sweden GB-0209474 holotype
Entoloma poliopus Estonia TUF120264
Entoloma meridionale Greece ACAM2018-0153 holotype
Entoloma riparium Italy L-0607563 holotype
Entoloma argus Vietnam LE F-312694 holotype
Entoloma icarus Vietnam LE F-312696 holotype
sect. Poliopodes subsct. Poliopodes
Entoloma sicoense Portugal PO-F2244 holotype
Entoloma sicoense Portugal PO-F2245
Entoloma mutabilipes Finland TUR610/12
sect. Poliopodes subsct.Mutabilipedes
Entoloma septentrionale Norway O-F-254295 holotype
sect. Poliopodes subsct.Allosperma
Entoloma chloropolium Estonia TUF120516
sect. Asprella subsct. Exilia 1
Entoloma queletii Turkey OKA-TR1002
Entoloma queletii Estonia TUF141044
sect. Caesiocincta subsct. Queletia
Entoloma callipygmaeum Russia LE253784 holotype
sect. Carneogrisea
Entoloma carneogriseum Norway O-F-256479
Entoloma subtenuicystidiatum China GDGM 28459 holotype
Entoloma arion Vietnam LE F-312691 holotype
Entoloma caespitosum China GDGM24025
Entoloma caespitosum China GDGM24026
Entoloma mastoideum China GDGM28820
Entoloma notabile Cyprus L-0607514 holotype
Entoloma linkii Norway O-F-256353
sect. Caesiocincta subsct. Caesiocincta
Entoloma zilin China HFJAU3354 holotype
Entoloma cyaneolilacinum Norway O-F-252009 holotype
sect.Asprella subsct. Cyaneolilacina
Entoloma timidum Russia LE 312480 holotype
Entoloma rivipollense Spain L-0607585 holotype
sect. Asprella subsct. Rivipollensia
Entoloma asprellum Estonia TUF106064
sect. Asprella subsct. Asprella
Entoloma exile Germany Lueck8
Entoloma exile USA KM187354
sect. Asprella subsct. Exilia 2
Entoloma qingluan China HFJAU5122 holotype
Entoloma qingluan China HFJAU5723
Entoloma cistocruentatum Spain L 0607521
sect. Asprella subsct. Cistocruentata
Entoloma perfidodiscum Spain L-0607586 holotype
sect. Asprella subsct. Perfidodisca
Entoloma pallidostriatum Spain L-0607566 holotype
sect. Caesiocincta subsct. Pallidostriata
Entoloma dislocatum Spain L0607565 holotype
sect. Caesiocincta subsct. Dislocata
Entoloma pulchripes Russia LE311808 holotype
Entoloma pulchripes Russia LE311809
Entoloma chalybeum Denmark TUF105760
Entoloma chalybeum Russia LE254353
sect. Chalybea
Entoloma incanum Sweden LE312503 neotype
Entoloma incanum Russia LE311794
sect. Fuliginosa subsct. Incana
Entoloma turci Austria WU25055
sect. Fuliginosa subsct. Turci
Entoloma perasprellum France GC01100310 holotype
sect. Atrocoerulea subsct. Perasprella
Entoloma griseocyaneum Germany KaiR997
Entoloma griseocyaneum Russia LE254351
sect. Griseocyanea subsct. Griseocyanea
Entoloma mougeotii Estonia TUF101633
Entoloma mougeotii Estonia TUF106505
sect. Griseocyanea subsct. Mougeotia
Entoloma cyanostipitum China GDGM31318 holotype
Entoloma pseudosubcorvinum Thailand SDBR-CMUNK0985 holotype
Entoloma azureosquamulosum China GDGM27355 holotype
Entoloma serrulatum Russia LE254361
Entoloma serrulatum Iran EnSe-1
sect. Cyanula subsct. Cyanula
Entoloma subcaesiocinctum China SAAS133 holotype
Entoloma coracis Norway O-F-256850 holotype
sect. Cyanula subsct. Coraces
Entoloma isborscanum Russia LE302088 holotype
sect. Cyanula subsct. Isborscana
Entoloma phlebophyllum China HFJAU3126
Entoloma murrayi China QI 1001
Entoloma kovalenkoi Vietnam LE312529
Entoloma cycneum Vietnam LE F-343654 holotype
outgroup
subg. Cyanula
subg. Cubospora
0.07

Figure 1. Phylogram of *Entoloma* subg. *Cyanula* spp. generated by Bayesian inference (BI) analysis based on ITS and LSU, rooted with *E.* subg. *Cubospora* spp. Bayesian inference (BI-PP) ≥ 0.95 and ML ultrafast bootstrap proportions (ML-BP) ≥ 95% are indicated as PP/BP. The new taxa are marked in bold.

moderately distant, 0.5–1.5 mm wide, adnate, ventricose, with two tiers of lamellae, paler greyish blue (21C5), edge serrate to crenate, concolorous. Stipe 7.0–16.5 × 1.2–2.0 mm, central, terete, slightly broadened downward, hollow, blue-black to dark blue or greyish blue (20E5–20D4), the surface is covered with white, velutinous to fibrillose-scales, base with white tomentum. Odor and taste not recorded.

Micromorphology. Basidiospores (7.5)8.5–10.5 × 6.5–8.0(8.5) µm, av = 9.4 × 7.2 µm, Q = 1.2–1.3 (Qm = 1.29 ± 0.03, n = 52), heterodiametrical, 5–7-angled in profile view, thick-walled, appearing nodulose, inamyloid. Basidia 37.0–54.5 × 9.0–12.5 µm, clavate, 4-spored. Pleurocystidia absent. Lamellae edge sterile, poliopus-type. Cheilocystidia clustered on lamella edge, 9.5–25.5 × 3.0–6.0 µm, narrowly clavate to subcylindrical. Lamellar trama regular, hyphae cells 3.5–6.0 µm wide. Pileipellis a trichoderm made up of clavate terminal cells, 5.5–16.0 µm, slightly constricted or level at the septa, with rounded or acute ends and dark brown vacuolar pigment. Stipitipellis transitional between cutis and trichoderm, composed of hyphae 4.0–8.0 µm wide, slightly constricted at septa, apices rounded, with brilliant granules abundant. Clamp connections absent.

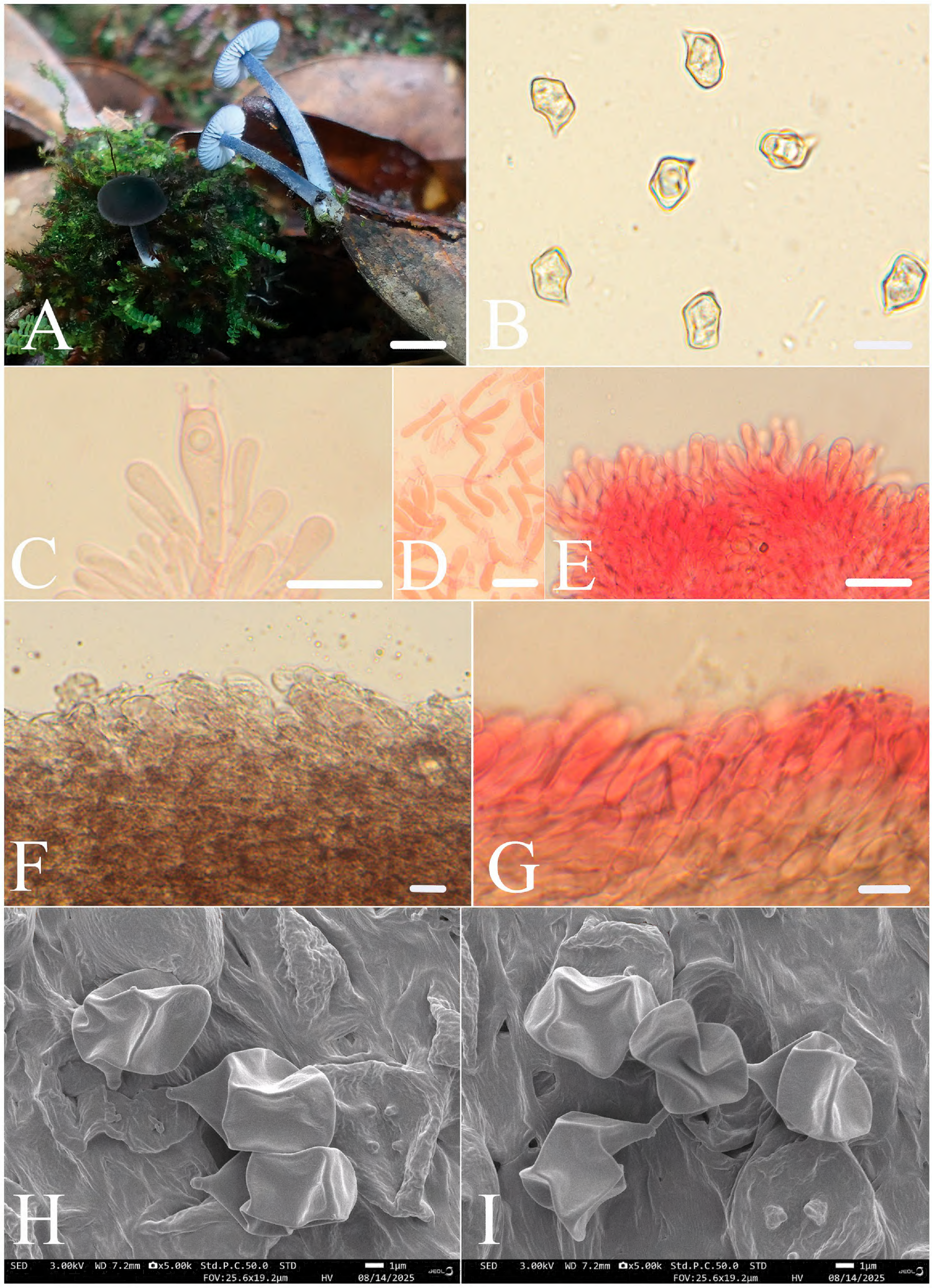

Figure 2. *Entoloma qingluan*. **A.** Basidiomata; **B, H, I.** Basidiospores; **C.** Basidia; **D, E.** Cheilocystidia; **F, G.** Pileipellis. All microscopic structures were observed in 5% KOH, and 1% Congo red was used as the stain except **F**. Scale bars: 5 mm (**A**); 10 µm (**B**); 20 µm (**C–E**); 10 µm (**F, G**).

Habitat. Scattered on mixed forest floors dominated by broad-leaved trees, such as *Pinus* spp. and *Pterocarya* spp.

Additional specimens examined. CHINA • Fujian Province, Wuyishan, 16 August 2023, collected by Nian-kai Zeng, Cheng-feng Nie, Hua-zhi Qin, Hui Deng, Tian Jiang, Run-xiang Zhao, HFJAU5723.

Notes. Considering the characteristics of this species, such as a darker-colored center on the pileus, blue stipe, and sterile lamella edges of the poliopus-type, this species can be classified into the subg. *Cyanula* sect. *Asprella* (Noordeloos et al. 2022a). However, it is impossible to classify *E. qingluan* into any of the subsections under this group based solely on morphological characteristics. Morphologically, this species is most similar to *E. cistocruentatum* Vila, Noordel. & Dima. However, *E. cistocruentatum* has fertile lamellae edges, lacks cheilocystidia, and possesses blue pigment in the pileipellis (Noordeloos et al. 2022b).

Morphologically, the new species is easily confused with *E. cyaneolilacinum* Noordel., J.B. Jordal, Brandrud & Dima. Both have a blue pileus and stipe, similar-sized spores, and brown vacuolar pigment in the pileipellis. However, the latter has a pileus with translucent stripes, emarginate lamellae that are white with a faint bluish tinge, fertile edges, and lacks cheilocystidia (Crous et al. 2021a). In addition, *E. azureosquamulosum* Xiao L. He & T.H. Li, discovered in southern China, also shows considerable similarity to this species. Both exhibit tricholomatoid basidiomata, with a blue pileus, adnate lamellae, sterile lamella edges, regular lamellar trama, and trichoderm pileipellis. However, *E. azureosquamulosum* has white to pink lamellae with a blue-tinged edge, fusoid cheilocystidia, and caulocystidia (He et al. 2012).

Entoloma zilin **J.Q. Yan, Y.Q. Xu & S.N. Wang, sp. nov.**

MycoBank No: 860912

Fig. 3

Etymology. The name “zilin” is derived from Hanyu Pinyin. The dark purple color of this species reminds people of the mythical zilin in Chinese legends, which is also depicted as dark purple.

Chinese name. 紫麟粉褶菌.

Holotype. CHINA • Zhejiang Province, Wenzhou City, Wencheng County, Yaping Hu, 25 May 2022, HFJAU3354.

Diagnosis. *Entoloma zilin* is mainly characterized by the rather small, collybioid basidiomata; pileus surface colored greyish-magenta which is covered with fibrous scales and is also striate; lamellae decurrent to slight sinuate, white with a bluish edge adjacent to the stipe; stipe blue; lamella edge fertile; cheilocystidia absent; pileipellis cells with sepia brown vacuolar pigment; clamp connections absent.

Macromorphology. Basidiomata small, collybioid. Pileus 8.0–10.0 mm wide, convex with slight central umbilicate depression, not hygrophanous, margin entire, surface densely covered with fibrous scales, greyish-magenta (14E6), margin and center dark purple (14F5), striate from the margin to the center. Lamellae moderately distant, decurrent to slight sinuate, white with a slight pinkish tinge, edge entire, bluish marginate adjacent to the stipe, with two tiers

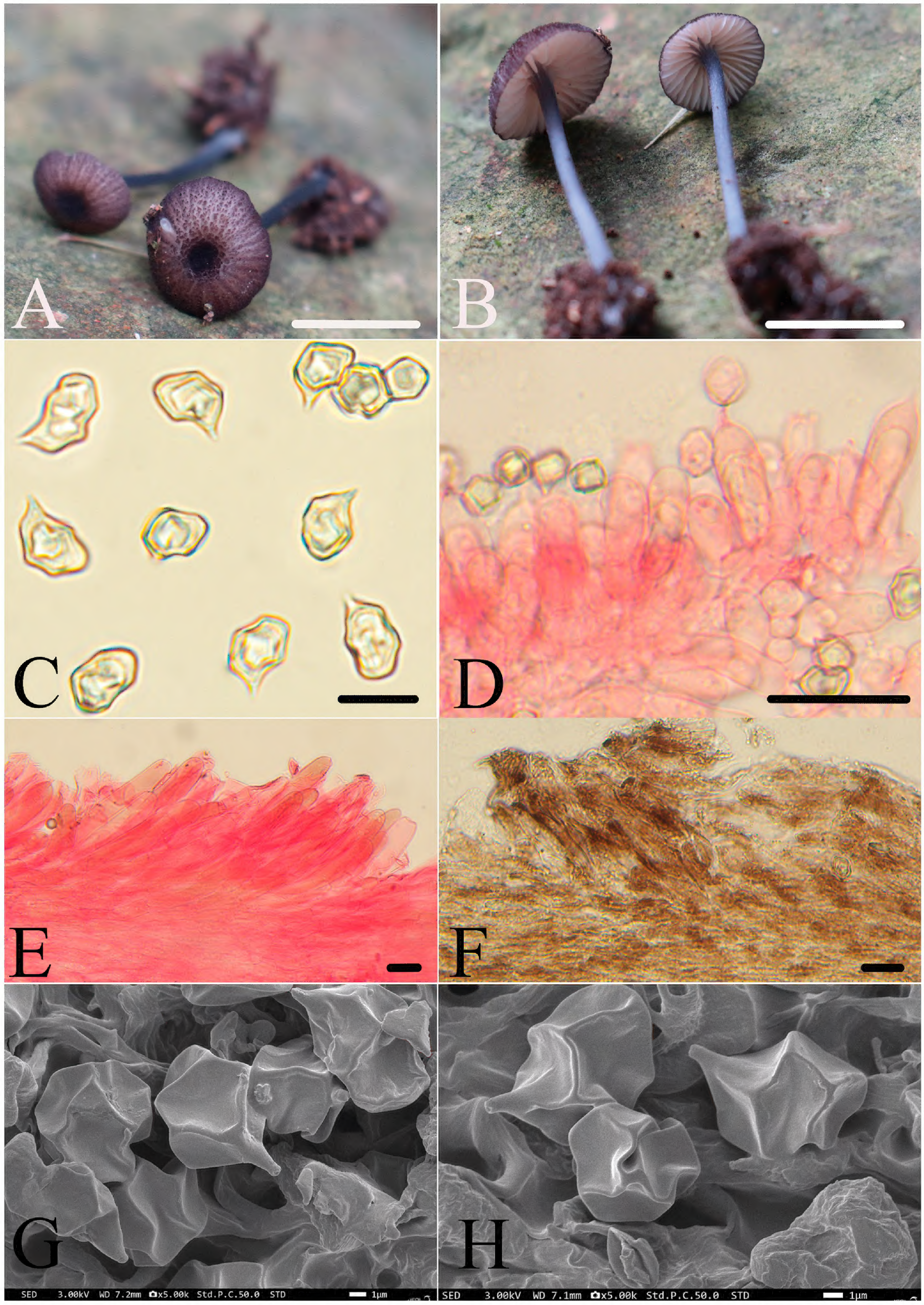

Figure 3. *Entoloma zilin*. **A, B.** Basidiomata; **C, G, H.** Basidiospores; **D.** Fertile lamella edge; **E, F.** Pileipellis. All microscopic structures were observed in 5% KOH, and 1% Congo red was used as the stain except **F**. Scale bars: 10 mm (**A–C**); 30 µm (**D**); 20 µm (**E, F**).

of lamellulae. Stipe 20.0–25.0 × 1.0–1.5 mm, central, terete, equal, hollow, dark blue (20E5); surface covered with white velutinous scales; base with white mycelium. Odor and taste not recorded.

Micromorphology. Basidiospores (8.5)9.0–12.0(13.0) × (6.5)7.0–8.5 µm, av = 10.7 × 7.6 µm, Q = 1.2–1.6(1.7) (Qm = 1.4 ± 0.1, n = 50), heterodiametrical, 5–8-angled in profile view, appearing nodulose, thick-walled, inamyloid. Basidia 29.0–41.0 × 7.0–12.0 µm, clavate, mainly 2-spored, rarely 4-spored. Lamellae edge fertile. Cheilocystidia and pleurocystidia absent. Lamellar trama regular. Pileipellis a trichoderm of cells 7.0–19.0 µm in diameter, cylindrical, slightly constricted at the septa, with cylindrical these terminal cells filled with sepia brown vacuolar pigment. Stipitipellis a cutis of densely arranged cylindrical hyphae 7.0–19.0 µm wide, slightly constricted at the septa, with terminal cells cylindrical to narrowly clavate and with rounded apices. Clamp connections absent.

Habitat. Scattered on the ground surface of broad-leaved forests and attached to the soil.

Notes. Based on the presence of scales and striations on the pileus surface, a blue stipe, and a fertile lamellae edge, the new species can be classified into sect. *Asprella* subsect. *Cyaneolilacina*. Only one species is known in this subsection: *E. cyaneolilacinum* Noordel., J.B. Jordal, Brandrud & Dima. However, it can be clearly distinguished from the new species by its deep blue to paler lilac-blue pileus, up to 25 mm in diam., and the absence of 2-spored basidia (Crous et al. 2021a).

The new species is morphologically similar to *E. violaceoviride* Arnolds & Noordel. Both have a greyish-magenta pileus with striations and scales. However, the latter has a papillate umbo on the pileus, adnexed lamellae that are initially violaceous then become violaceous-pink, and a stipe that is pale greyish green at first, and then gradually changes from the base upward to bluish-grey with a greenish tinge, with the apex remaining pale green, as well as sterile lamellae edges (Noordeloos 2004). In addition, the new species also shares certain similarities with *E. melongenicolor* Noordel. & Hauskn. from Africa (Mahé Island, Seychelles). Both have umbilicate pileus centers, blue stipes, similarly sized spores, fertile lamellae edges, and cheilocystidia absent. However, the latter has an aubergine-colored pileus, pale brick-red lamellae, and a pileipellis with bluish-brown vacuolar pigment (Noordeloos and Hausknecht 2016).

Discussion

In this study, the two newly discovered species, *E. qingluan* and *E. zilin*, each form an independent and well-supported branch in the phylogenetic tree based on ITS and LSU sequences and are therefore considered genetically distinct from their closest relatives. Morphologically, both new species can be classified as sect. *Asprella*. Nevertheless, sect. *Asprella* is not recovered as a monophyletic clade: *E. zilin* nests within sect. *Asprella* subsect. *Cyaneolilacina* alongside *E. cyaneolilacinum*, whereas *E. qingluan* clusters with *E. exile* (sect. *Exilia*). The morphological differences between *E. zilin* and *E. cyaneolilacinum* have been discussed in the notes. *Entoloma qingluan* is easily separated from *E. exile* by its blue-grey to blue-black pileus and stipe; *E. exile* has a yellow-brown or grey-brown pileus, often with olivaceous or whitish tints, and its stipe turns red when bruised.

At the sectional level, subgenus *Cyanula* displays extensive incongruence between morphology and molecular phylogeny. Section *Asprella* is resolved as polyphyletic, and the same applies to sections *Poliopodes* and *Caesiocincta*. In addition, numerous taxa cannot yet be assigned to defined sections or subsections. To refine intrasectional delimitation, additional loci, broader sampling, and continued discovery of new taxa are imperative. Only by integrating molecular and morphological data can the current polyphyletic structure of subgenus *Cyanula* be resolved. The present study enhances our understanding of the diversity of this subgenus in China.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Conceptualization, Jun-Qing Yan; methodology, Jun-Qing Yan and Sheng-Nan Wang; software, Yu-Qin Xu; formal analysis, Hui Zeng, Jun-Qing Yan, and Sheng-Nan Wang; investigation, Yu-Qin Xu and Jun-Qing Yan; resources, Hui Zeng, Liu-Hua Guo, and Jun-Qing Yan; writing—original draft, Yu-Qin Xu; writing—review and editing, Jun-Qing Yan; visualization, Jun-Qing Yan and Sheng-Nan Wang; supervision, Jun-Qing Yan; project administration, Jun-Qing Yan; funding acquisition, Jun-Qing Yan. All authors have read and agreed to the published version of the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text.

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